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procedure to maximize the value of oligonucleotide microarray expression profiles.

Design, methods, and results:

Background microarray noise was 82.2 ± 54.5 and 51.8 ± 12.4 units, respectively, before and after enacting the program (P < 0.0001). We also noted improved concordance of microarray expression foldchanges for selected genes with results of RT-PCR validation.

Conclusions:

This multi-step procedure, including quantification of RNA sample degradation and detection of outlier data points, has increased data quality from our microarray facility.

Keywords: RNA; Oligonucleotide microarrays; Data quality; Gene expression: Microarray analysis

Article Outline

Introduction

Methods

RNA quality analysis

Quality control after cRNA labeling and hybridization

Results

Performance improvement over time Microarray validation with RT-PCR

Conclusion Acknowledgements

References

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